FILE 'MEDLINE, HCAPLUS, BIOSIS, USPATFULL, WPIDS' ENTERED AT 13:38:00 ON 08 FEB 2000

L68	428	S ZENTGRAF H?/AU
L69	403	S POUSTKA A?/AU
L70	144	S COY J?/AU
L71	23	S VELHAGEN I?/AU
L72	3	S L68 AND L69 AND L70 AND L71
L73	2	DUP REM L72 (1 DUPLICATE REMOVED) 2 cites
L74	930	S L68-71
L75	23	S L74 AND (DNASE OR APOPTOSIS)
L76	20	S L75 NOT L72
L77	11	DUP REM L76 (9 DUPLICATES REMOVED) 11 cites

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=> d sqide 14

L4   ANSWER 1 OF 2  REGISTRY  COPYRIGHT 2000 ACS
RN   197100-17-7  REGISTRY
CN   Tumor necrosis factor .epsilon. (human) (9CI)  (CA INDEX NAME)
FS   PROTEIN SEQUENCE
SQL  168

SEQ      1 GTGGPSQNGE GYPWQSLPEQ SSDALEAWES GERSRKRRAV LTQKQKNDSD
        51 VTEVMWQPAL RRGRGLQAQG YGVRIQDAGV YLLYSQVLFQ DVTFTMGQVV
       101 SREGQGRQET LFRCIRSMPS HPDRAYNSCY SAGVFHLHQG DILSVIIPRA
       151 RAKLNLSPHG TFLGFVKL
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS
                1 REFERENCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1967 TO DATE)


=> d sqide 14 2

L4   ANSWER 2 OF 2  REGISTRY  COPYRIGHT 2000 ACS
RN   197100-15-5  REGISTRY
CN   Tumor necrosis factor .delta. (human clone pBacTNFdelta) (9CI)  (CA INDEX
     NAME)
FS   PROTEIN SEQUENCE
SQL  230

SEQ      1 MGGPVREPAL SVALWLSWGA ALGAVACAMA LLTQQTELQS LRREVSRLQR
        51 TGGPSQNGEG YPWQSLPEQS SDALEAWENG ERSRKRRAVL TQKQKEQHSV
       101 LHLVPINATS KDDSDVTEVM WQPALRRGRG LQAQGYGVRI QDAGVYLLYS
       151 QVLFQDVTFT MGQVVSREGQ GRQETLFRCI RSMPSHPDRA YNSCYSAGVF
       201 HLHQGDILSV IIPRARAFLN LSPHGTFLGF
MF   Unspecified
CI   MAN
SR   CA
LC   STN Files:   CA, CAPLUS
                1 REFERENCES IN FILE CA (1967 TO DATE)
                1 REFERENCES IN FILE CAPLUS (1967 TO DATE)


=> d bib abs l73

L73  ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2000 ACS        DUPLICATE 1
AN   1996:567285  HCAPLUS
DN   125:185869
TI   Human chromosome X region q27.3 DNase cDNA sequence, antibody specific for
     DNase, and diagnosis and therapy of apoptosis-related diseases such as
     cancer
IN   Zentgraf, hanswalter; Poustka, Annemarie; Coy,
     Johannes; Velhagen, Iris
PA   Deutsches Krebsforschungszentrum Stiftung des Oeffentlichen Rechts,
     Germany
SO   Ger., 6 pp.
     CODEN: GWXXAW
DT   Patent
LA   German
FAN.CNT 1
     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ---------------   ----  --------      ---------------  --------
PI   DE 19521046        C1   19960808      DE 1995-19521046 19950609
     WO 9641887         A1   19961227      WO 1996-DE1016   19960610
         W:  JP, US
         RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
     EP 842278          A1   19980520      EP 1996-915989   19960610
         R:  AT, BE, CH, DE, DK, ES, FR, GB, IT, LI, NL, SE
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JP 11507825 T2 19990713 JP 1996-502488 19960610
PRAI DE 1995-19521046 19950609
WO 1996-DE1016 19960610

AB A DNase gene was found on human chromosome in the q27.3 region and its cDNA sequence is shown. This invention comprises the DNase, the gene encoding DNase, and an antibody specific for the DNase. Recombinant enzyme prodn., transformant gene expression, and use in diagnosis and therapy of apoptosis-related diseases, such as cancer, are included.

=> d bib abs l73 2

L73 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2000 ACS
AN 1996:489924 HCAPLUS
DN 125:160037
TI Isolation, differential splicing and protein expression of a DNase on the human X chromosome
AU **Coy, Johannes F.**; **Velhagen, Iris**; Himmele, Rainer; Delius, Hajo; **Poustka, Annemarie**; **Zentgraf, Hanswalter**
CS Deutsches Krebstorschungszentrum, Abteilung Molekulare Genomanalyse, Heidelberg, 69120, Germany
SO Cell Death Differ. (1996), 3(2), 199-206
CODEN: CDDIEK; ISSN: 1350-9047
DT Journal
LA English
AB A systematic search for genes differentially expressed in human tissues resulted in the isolation of a gene encoding a protein with high homol. to DNase 1. In addn. to the recently described cDNA sequence (Parrish et al., 1995) the authors have isolated a transcript, alternatively spliced in the 5' noncoding region. The gene is located between the QM and the XAP-2 gene in Xq28 and encodes a 302 amino acid protein with 39% identity to human DNase 1. Besides a high homol. at the nucleotide and amino acid level, most exon-intron boundaries of DNase 1 and DNase X are identical, indicating that both genes may have evolved from a common ancestor. The predicted function was verified by expression of a recombinant protein in an inducible bacterial system and detection of DNase activity. In contrast to DNase 1 a 18 kDa amino terminal fragment of the full length 35 kDa protein exhibited DNase activity.

=> d bib abs l77 1-11

L77 ANSWER 1 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1999:510638 BIOSIS
DN PREV199900510638
TI Fas ligand expression in the germinal centre.
AU Verbeke, Caroline S. (1); Wenthe, Ursula; **Zentgraf, Hanswalter**
CS (1) Fakultaet fuer Klinische Medizin Mannheim der Universitaet Heidelberg, Pathologisches Universitaetsinstitut, Th.-Kutzer-Ufer 1, 68167, Mannheim Germany
SO Journal of Pathology, (Oct., 1999) Vol. 189, No. 2, pp. 155-160. ISSN: 0022-3417.
DT Article
LA English
SL English
AB Whereas the importance of the Fas/FasL system in the regulation of T-cell homeostasis is well established, it is not yet clear if FasL is involved in B-cell regulation, especially in the clonal selection of B lymphocytes in the germinal centre (GC). This study therefore investigated the expression of FasL protein in tonsils and lymph nodes with lymphofollicular hyperplasia by western blotting and immunohistochemistry. In all the samples examined, western blot analysis showed FasL proteins of 33 and 52 kD, which presumably correspond to membrane-bound and soluble forms of the FasL protein. Immunohistochemically, FasL was found in a limited number of cells confined to a cluster in the light zone of the GC. The signal showed a delicate meshwork-like pattern of branching processes enmeshing the centrocytes and the few centroblasts of the light zone. In serial sections, the immunostaining pattern for FasL was found largely to coincide with the CD23 staining of follicular dendritic cells (FDCs), which are typically located in the light zone. In contrast, the FasL signal did not correspond to the distribution of the CD4-positive GC T-cells. In conclusion, expression of FasL in lymphofollicular hyperplasia seems to be largely confined to the light zone of the GCs, where selection of FDC-associated centrocytes is known to occur. These observations thus suggest that FasL is involved in selection processes of the B-cell system.

L77 ANSWER 2 OF 11 HCAPLUS COPYRIGHT 2000 ACS
AN 1999:608048 HCAPLUS
DN 131:349215
TI Dickkopf genes are co-ordinately expressed in mesodermal lineages
AU Monaghan, A. P.; Kioschis, P.; Wu, W.; Zuniga, A.; Bock, D.; **Poustka, A.**; Delius, H.; Niehrs, C.
CS Division of Molecular Genome Analysis, Deutsches Krebsforschungszentrum, Heidelberg, D-69120, Germany
SO Mech. Dev. (1999), 87(1,2), 45-56
CODEN: MEDVE6; ISSN: 0925-4773
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Dickkopf-1 (dkk-1) is member of a novel family of secreted proteins and functions in head induction during Xenopus embryogenesis, acting as a potent inhibitor of Wnt signaling. Here we report: (1) the isolation of 2 addnl. murine members of the dkk family, dkk-2 and dkk-3; and (2) anal. of adult and embryonic gene expression of mouse dkk-1,-2, and -3, Xenopus dkk-1 as well as chicken dkk-3. Comparative developmental analyses of the dkk-1, dkk-2, and dkk-3 in mice indicate that these genes are both temporally and spatially regulated. They define overlapping deep domains in mesenchymal lineages suggesting a coordinated mode of action. All dkks show distinct and elevated expression patterns in tissues that mediate epithelial-mesenchyme transformations suggesting that they may participate in heart, tooth, hair and whisker follicle, limb and bone induction. In the limb buds expression of these genes are found in regions of programmed cell death. In a given organ, dkk-1 tends to be the earliest member expressed. Comparison with Xenopus dkk-1 and chicken dkk-3 shows evolutionarily conserved expression patterns. Our observations indicate that dkk genes constitute a new family of secreted proteins that may mediate inductive interactions between epithelial and mesenchymal cells.

L77 ANSWER 3 OF 11 MEDLINE DUPLICATE 1

AN 1998373989 MEDLINE
DN 98373989
TI A regulatory element in the CD95 (APO-1/Fas) ligand promoter is essential for responsiveness to TCR-mediated activation.
AU Li-Weber M; Laur O; Hekele A; **Coy J**; Walczak H; Krammer P H
CS Tumor Immunology Program, German Cancer Research Center, Heidelberg.. m.li-weber@dkfz-heidelberg.de
SO EUROPEAN JOURNAL OF IMMUNOLOGY, (1998 Aug) 28 (8) 2373-83. Journal code: EN5. ISSN: 0014-2980.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199811
EW 19981101
AB Expression of the CD95 (APO-1/Fas) ligand (CD95L) in activated T cells is a major cause of T cell activation-induced **apoptosis**. To study the molecular mechanisms of transcriptional control of CD95L expression in T cells, we investigated the human CD95L promoter in Jurkat T cells. Deletion studies revealed that the CD95L proximal promoter sequence from -220 to the transcription start site is essential for T cell stimulation-induced expression of CD95L. In this study, we discovered a novel regulatory element located at -120 of the CD95L promoter which contains DNA binding sites for SP-1 and a yet unknown inducible factor. Mutation analysis demonstrated that binding of the inducible factor to the -120 region is crucial for the biological function of the CD95L promoter upon T cell stimulation. The DNA sequence at -120 also contains two DNA motifs homologous to the binding site for NF-AT. NF-AT does not directly bind to this element. However, cotransfection studies with an NF-AT expression vector showed that NF-AT may confer a strong inducible activity to the CD95L promoter at this regulatory region. Our data also show that the immunosuppressive agent cyclosporin A down-regulates CD95L transcription by inhibiting the function of this positive regulatory element.

L77 ANSWER 4 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1997:53256 BIOSIS
DN PREV199799352459
TI Activation of **DNase** X: A new candidate enzyme mediating DNA fragmentation during **apoptosis**.
AU Los, M.; **Coy, J.**; Walczak, H.; Debatin, K.-M.
CS Hematol./Oncol., Univ. Child. Hosp., Im Neuenheimer Feld 150, Heidelberg Germany
SO Blood, (1996) Vol. 88, No. 10 SUPPL. 1 PART 1-2, pp. 69A. Meeting Info.: Thirty-eighth Annual Meeting of the American Society of Hematology Orlando, Florida, USA December 6-10, 1996 ISSN: 0006-4971.
DT Conference; Abstract; Conference
LA English

L77 ANSWER 5 OF 11 HCAPLUS COPYRIGHT 2000 ACS
AN 1988:200619 HCAPLUS
DN 108:200619
TI The duck hepatitis B virus DNA polymerase is tightly associated with the viral core structure and unable to switch to an exogenous template
AU Radziwill, Gerald; **Zentgraf, Hanswalter**; Schaller, Heinz; Bosch, Valerie
CS Microbiol. ZMBH, Univ. Heidelberg, Heidelberg, 6900, Fed. Rep. Ger.
SO Virology (1988), 163(1), 123-32 CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB The duck hepatitis B virus (DHBV) has a DNA polymerase assocd. with it which uses the incomplete viral genome as endogenous template. A prerequisite for studying this polymerase is the availability of conditions to open viral cores without destroying their enzymic activity. In this study, this was achieved by a brief treatment with low pH. DHBV DNA in low-pH-treated cores was susceptible to digestion with **DNase** I and restriction enzymes, and large restriction fragments diffused out of the viral cores. However, the DHBV polymerase remained

tightly assocd. with its DNA template in the viral core structure and could still incorporate nucleotides into those DNA fragments which carried the DNA-bound protein and remained in the core. The DHBV polymerase could not switch to any of several exogenously supplied templates although these were most likely accessible to it. The manner in which this tight assocn. of the DHBV polymerase with the core may occur, and the possible implications of this interaction during the DHBV replication cycle, is discussed.

L77 ANSWER 6 OF 11 MEDLINE DUPLICATE 2
AN 86200394 MEDLINE
DN 86200394
TI Properties of intracellular bovine papillomavirus chromatin.
AU Rosl F; Waldeck W; **Zentgraf H**; Sauer G
SO JOURNAL OF VIROLOGY, (1986 May) 58 (2) 500-7.
Journal code: KCV. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 198608
AB Episomal nucleoprotein complexes of bovine papillomavirus type 1 (BPV-1) in transformed cells were exposed to **DNase** I treatment to localize hypersensitive regions. Such regions, which are indicative for gene expression, were found within the noncoding part of the genome, coinciding with the origin of replication and the 5' ends of most of the early mRNAs. However, there were also regions of hypersensitivity within the structural genes. These intragenic perturbations of the chromatin structure coincide with regulatory sequences at the DNA level. One of these regions maps in close proximity to a Z-DNA antibody-binding site which is located near the putative BPV-1 enhancer sequence.

L77 ANSWER 7 OF 11 MEDLINE DUPLICATE 3
AN 85027172 MEDLINE
DN 85027172
TI Origin of replication in episomal bovine papilloma virus type 1 DNA isolated from transformed cells.
AU Waldeck W; Rosl F; **Zentgraf H**
SO EMBO JOURNAL, (1984 Sep) 3 (9) 2173-8.
Journal code: EMB. ISSN: 0261-4189.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198502
AB The origin of replication of bovine papilloma virus type 1 (BPV-1) has been determined by isolating replicative intermediates (RI) of BPV-transformed hamster embryo fibroblasts (HEF-BPV). These RI were treated with single cut restriction enzymes to determine the start-position (origin) of the extending replication eyes using electron microscopic techniques. 'Cairns'-type RI molecules were shown to contain one replication eye in monomeric as well as in dimeric molecules. The position of this eye was localized at 6940 +/- 5% bp in the physical map. In a second set of experiments BPV-1 DNA fragments cloned in pBR322 were tested for transient episomal replication. Transfected cells were harvested after increasing periods of time and screened for replication with isoschizomeric restriction enzymes to differentiate between input and replicated DNA. The part of the BPV genome harboring the replication origin spans the BPV ClaI-C restriction fragment corresponding to the non-coding region of the BPV genome and coincides with the **DNase** I-hypersensitive control region in the chromatin, isolated from transformed cells.

L77 ANSWER 8 OF 11 MEDLINE DUPLICATE 4
AN 82116483 MEDLINE
DN 82116483
TI Different chromatin structures in Physarum polycephalum: a special form of transcriptionally active chromatin devoid of nucleosomal particles.
AU Scheer U; **Zentgraf H**; Sauer H W
SO CHROMOSOMA, (1981) 84 (2) 279-90.

Journal code: D7A. ISSN: 0009-5915.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198206
AB Nonnucleolar chromatin from interphase nuclei of Physarum polycephalum plasmodia occurs in two different structural configurations as seen in electron microscopic spread preparations. While the majority of the chromatin is devoid of nascent ribonucleoprotein (RNP) fibrils and compacted into nucleosomal particles, a minor proportion (10-20%) is organized differently and reveals a smooth contour. It is this form of smooth chromatin which is rich in transcription units (mean length: 1.36 +/- 0.21 micrometer). Only occasionally are solitary nascent RNP fibrils observed which are associated with beaded strands of chromatin. In transcribed smooth chromatin nucleosomal particles are not only absent from the transcription units but also from their nontranscribed flanking regions, indicating that this special structural aspect is not merely a direct consequence of the transcriptional process. The existence of ca. 10-20% of Physarum chromatin in the smoothly contoured form is discussed in relation to reports of a preferential digestibility of a similar proportion of Physarum chromatin by **DNAse** I (Jalouzot et al., 1980) and to the altered configuration of "peak A" chromatin subunits after micrococcal nuclease digestion (Johnson et al., 1978 a, b).

L77 ANSWER 9 OF 11 BIOSIS COPYRIGHT 2000 BIOSIS
AN 1979:58505 BIOSIS
DN BR16:58505
TI MORPHOLOGY OF TRANSCRIPTIONALLY ACTIVE CHROMATIN.
AU FRANKE W W; SCHEER U; TRENDELENBURG M; **ZENTGRAF H**; SPRING H
SO COLD SPRING HARBOR LAB. COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, VOL. 42. CHROMATIN. PART 1 AND 2. COLD SPRING HARBOR, N.Y., USA, JUNE 1-8, 1977. XXII+603P.(PART 1); XXII+657P.(PART 2). COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR, N.Y., USA. (1978) 755-772.
ISBN: 0-87969-041-0.
FS BR; OLD
LA Unavailable

L77 ANSWER 10 OF 11 HCAPLUS COPYRIGHT 2000 ACS DUPLICATE 5
AN 1973:543616 HCAPLUS
DN 79:143616
TI Nuclear membranes from mammalian liver. IV. Characterization of membrane-attached DNA
AU Franke, W. W.; Deumling, Barbara; **Zentgraf, H.**; Falk, H.; Rae, P. M. M.
CS Inst. Biol. II, Univ. Freiburg/Br., Freiburg/Br., Ger.
SO Exp. Cell Res. (1973), 81(2), 365-92
CODEN: ECREAL
DT Journal
LA English
AB DNA assocd. with nuclear membranes isolated from liver tissue of mice and rats (sucklings and partially hepatectomized adults) was analyzed and directly demonstrated by electron microscopy using spreading techniques. The sensitivity of this DNA-membrane assocn. to **DNAse**, 4M CsCl centrifugation, urea, and detergent was examd. and compared with that of microsomal DNA. The DNA was purified from nuclear membrane fractions, and the purity and mol. size distribution of the prepns. were detd. The characteristics of this DNA with respect to buoyant d., melting behavior, content of repetitive sequences, nucleotide compn., mol. configuration, and turnover and labeling kinetics with various precursors (thymidine, deoxycytidine, phosphate) were examd. and compared with the corresponding properties of DNA from whole nuclei and other nuclear subfractions. Most properties of membrane DNA were identical or similar to those of bulk nuclear DNA. It was, however, enriched in satelite DNA and other repetitive sequences to a moderate extent and differed from it in its replication rate and time. The results reflect the close relation between the nuclear envelope and (constitutive) heterochromatin, but also indicate that membrane binding is not restricted to this material. A preferential localization of replicating points in the nuclear membrane DNA, as well as an initiation of replication at the nuclear envelope are argued against.

L77 ANSWER 11 OF 11 HCAPLUS COPYRIGHT 2000 ACS
AN 1971:137065 HCAPLUS
DN 74:137065
TI Nuclear membranes and plasma membranes from hen erythrocytes. I. Isolation, characterization, and comparison
AU **Zentgraf, Hanswalter**; Deumling, Barbara; Jarasch, Ernst D.; Franke, Werner W.
CS Inst. Biol. II, Univ. Freiburg, Freiburg/Br., Ger.
SO J. Biol. Chem. (1971), 246(9), 2986-95
CODEN: JBCHA3
DT Journal
LA English
AB The bird erythrocyte provides a cell system which comprises only 2 sorts of membranes, namely the plasma membrane and the nuclear envelope. As calcd. morphometrically, both of these membranes are present in an almost 1:1 membrane surface ratio. Contamination with other types of membranes is a priori excluded in this cell. Purified fractions of plasma membranes and nuclear envelope membranes were isolated by using nondetergent methods, in which high speed rotating knife homogenization is combined with differential and gradient centrifugation steps. Nuclear membranes were sepd. from other nuclear constituents after high salt extn. of nucleoproteins and sonic oscillation, with or without an addnl. digestion with **DNase**. Purity and structural integrity of the fractions are shown in electron micrographs. The buoyant densities of nuclear membranes (.rho.422 = 1.20) and plasma membranes (.rho.422 = 1.14) are different. The gross compns. of intact cells and the nuclei, nuclear membrane, and plasma membrane fractions, with respect to lipids, phospholipids, cholesterol, protein, RNA, and DNA, are given, as well as corresponding recoveries. The nuclear membrane is distinct from the plasma membrane as shown in a much lower cholesterol-phospholipid ratio, in a higher content in protein, and a certain amt. of DNA remaining firmly attached to it.